

KEYWORDS	EST.	us-09-817-869-2.1st	Page 4
KEYWORDS	Gossypium arboreum.		
SOURCE	Gossypium arboreum.		
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REFERENCE	1 (bases 1 to 909)		
AUTHORS	Wang, R.A., Fritch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, J.B., Wood, T.C., Leslie, D.A., and Wilkins, T.A.		
TITLE	An integrated analysis of the genetics, development, and evolution of cotton		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Wang RA Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Email: rfwang@clemson.edu Seq primer: TAATACACTACTATAGAG High quality sequence stop: 755. Local/Qualifiers		
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AUTHORS	Anderson, O.A., Appels, R., Bailey, P., Blake, I., Close, T., Cloutier			
	S., Dubrovsky, J., Foullet, C., Gale, M., Graner, A., Gustafson, P.,			
	Herrmann, R.G., Holtorf, T., Jacquemin, J.M., Jia, J., Joudrier, P.,			
	Kammann, R.P., Lazo, G.R., Lind, J., McGuire, P., Quahar, Y.,			
	Rendall, M., Schach, M., Sevelin, J.G., Shariflou, M.,			
	Sorrells, M., Warburton, M., Wenzel, G.			
TITLE	International Triticeae EST Cooperative (ITEC): Production of			
	Expressed Sequence Tags for Species of the Triticeae			
COMMENT	Unpublished (2000)			
	Contact: Graner A			
	Institute for Plant Genetics & Crop Plant Research			
	Corrensstr. 3, D-06466 Gatersleben GERMANY			
	Tel: 49 34482 51121			
	Fax: 49 34482 51119			
	Email: a.graner@ipk.gatersleben.de			
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FEATURES				

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Search completed: May 5, 2003, 07:20:29
Job time : 4729.93 secs




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RESUME 14
US-09-878-574-8442
? Sequence 1442, Application US/09/87874
? Patent No. US2002011054A1
? GENERAL INFORMATION:
? APPLICANT: Hyatt, Joseph R.
? APPLICANT: Thompson, Michael D.
? APPLICANT: La Rosa, Thomas J.
? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
? FILE REFERENCE: 48-21(140)19
? CURRENT APPLICATION NUMBER: US/09/878,574
? PRIOR FILING DATE: 2001-12-21
? PRIOR FILING DATE: 1994-06-14
? PRIOR FILING DATE: 1994-06-14
? NUMBER OF SEQ ID NOS: 15775
? SEQ ID NO: 442
? TYPE: DNA
? ORGANISM: E. coli
? OTHER INFORMATION: Clone ID: L18402B-010-Q1-R1-B9
US-09-878-574-3442

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DB 97 CATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 156
QY 219 CATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 296
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US-09-878-574-8447
? Sequence 8447, Application US/09/87874
? Patent No. US2002011054A1
? GENERAL INFORMATION:
? APPLICANT: Hyatt, Joseph R.
? APPLICANT: Thompson, Michael D.
? APPLICANT: La Rosa, Thomas J.
? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
? FILE REFERENCE: 48-21(140)19
? CURRENT APPLICATION NUMBER: US/09/878,574
? PRIOR FILING DATE: 2001-12-21
? PRIOR FILING DATE: 1994-06-14
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? ORGANISM: E. coli
? OTHER INFORMATION: Clone ID: P011012101
US-09-878-574-8447

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DB 61 CATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
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GenInfo version 5.1.5
Copyright (c) 1991 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
5618.756 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0

Searched: 441638 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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					Sequence 19, Appl
					Sequence 20, Appl
					Sequence 21, Appl
					Sequence 22, Appl
					Sequence 23, Appl
					Sequence 24, Appl
					Sequence 25, Appl
					Sequence 26, Appl
					Sequence 27, Appl

Sequence 1, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 8, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-471-251A-1
Sequence 1, Application US/08471251A
Patent No. 5,618,756
GENERAL INFORMATION:
APPLICANT: Wang, Xuebin
TITLE OF INVENTION: RECOMBINANT DNA SEQUENCES ENCODING
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John M. Collins, Bovey, Williams, Timmons &
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
FILE NAME: US08471251A.DAT
OPERATING SYSTEM: PC/INSTRANS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08471251A
FILING DATE: June 6, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
FIRM: Collins, Bovey, Williams, Timmons &
REGISTRATION NUMBER: 24262
REFERENCE/DOCKET NUMBER: 24703
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9057
TELEFAX: (816) 474-9057
INFORMATION FOR SPO ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE TYPE: double
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: circular
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-471-251A-1

Query Match 97.28: Score 2728.4: tw 1: Length 2804:
Host Local Similarity 99.18: Pred. No. 0:
Matches 2785: Conservative 0: Mismatches 21: Indels 4: Gaps 4:
Oy 1 CTTGATTTCACATTCTCTGTTTATATAGGACATACAAATATATTTTATTCAT 60
1 CTTGATTTCACATTCTCTGTTTATATAGGACATACAAATATATTTTATTCAT 60


```

; MOLECULE TYPE: cDNA to mRNA
;
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 182..2617
US-08-750-007-2

```

Query Match 48.9%; Score 1373.8; DB 1; Length 3040;

[illegible]


```

: NAME/KEY: CDS
: LOCATION: 1..3108
US-08-968-752B-3

Query Match 1.5% Score 41.4; DB 3; Length 3108;
Best local Similarity 62.4%; Prod. No. 0.0071;
Matches 68; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 2127 TCATTATGTCATCAACAAGATGTCGTCGATGATGACATATATATGATCTG 2186
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2561 TTATATGTCGACACCAAGTGTATATGTCGATGACATATGTCGATCTG 2620
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2187 CCACATCAACACAGATATGATGATGTCGATGACATATGTCGATCTG 2245
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2621 CCACATCAACACAGATATGATGATGTCGATGACATATGTCGATCTG 2785
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
: Sequence 1B, Application US/09107149
: Patent No. 6274563
: GENERAL INFORMATION:
: APPLICANT: Frohman, David W.
: APPLICANT: Tomkins, Christopher K.
: TITLE OF INVENTION: PHOSPHOLIPASE D PHOSPHOLIPASE D
: FILE REFERENCE: 077319/0144
: CURRENT APPLICATION NUMBER: US/09/107,149
: CURRENT FILING DATE: 1998-06-30
: PRIORITY APPLICATION NUMBER: 06/766,147
: PRIORITY FILING DATE: 1998-12-17
: NUMBER OF SEQ. ID NOS.: 25
: SOFTWARE: Patent In Ver. 2.0
: SEQ. ID NO. 18
: LENGTH: 4114
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: CDS
: LOCUS: (52) .. (2964)
US-09-107-149-18

Query Match 1.5% Score 41.4; DB 4; Length 4114;
Best Local Similarity 62.4%; Prod. No. 0.0071;
Matches 68; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 2127 TCATTATGTCATCAACAAGATGTCGATGATGACATATATGATCTG 2186
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2561 TTATATGTCGACACCAAGTGTATATGTCGATGACATATGTCGATCTG 2620
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2187 CCACATCAACACAGATATGATGATGTCGATGACATATGTCGATCTG 2245
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2621 CCACATCAACACAGATATGATGATGTCGATGACATATGTCGATCTG 2785
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-08-968-752B-1
: Sequence 1, Application US/89687528
: Patent No. 6043074
: GENERAL INFORMATION:
: APPLICANT: Frohman, Michael A.
: APPLICANT: Morris, Andrew
: TITLE OF INVENTION: Phospholipase D Polypeptide and
: TITLE OF INVENTION: DNA Sequences
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSED: ONYX Pharmaceuticals, Inc.
: STREET: 3031 Research Drive
: CITY: Richmond
: STATE: California
: COUNTRY: USA
: ZIP: 94806
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.0
: CURRENT APPLICATION NUMBER: US/08/968,752B
: FILING DATE: 13-AUG-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/025,469
: FILING DATE: 05-SEP-1996

```

```

1 ATTORNEY/AGENT INFORMATION:
2 NAME: Gloria, Gregory J.
3 REGISTRATION NUMBER: 42,028
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 510-222-9700
6 TELEFAX: 510-222-9758
7 INFORMATION FOR SEQ ID NO: 1:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 4222 base pairs
10 TYPE: nucleic acid
11 TOPOLOGY: double
12 MOLECULE TYPE: cDNA
13 HYDROTICAL: NO
14 ANTI-SENSE: NO
15 FEATURE:
16 NAME/KEY: CDS
17 LOCATION: 1..3222
18 US-09-546-224-1
19
20 Query Match
21 best Local Similarity 62.48; Pval 8e-007;
22 Matches 68; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
23
24 QY 2127 TATTTATGTTTAAACAAGATGATGCTGATGATGAGTAAATATATATGATGCTG 2186
25 DB 2675 TTATCTATGTCACAGCAACTGTTTAATGCTGTATGATTAACATGTTATTAAGCTG 2714
26
27 QY 2187 GCAACAATCAACATGATCAATGATGCTGTAGATGATGCAAAATAGC 4245
28 DB 2745 GCAACAATCAACATGATGATGCTGTGGAAGATGCTGCAAAATAGC 2783
29
30 RESULT 14
31 US-09-546-224-1
32 Sequence 1, Application US/09536224
33 Patent No. 6479665
34 GENERAL INFORMATION:
35 APPLICANT: Frohman, Michael A.
36 APPLICANT: Morris, Andrew
37 TITLE OF INVENTION: DNA Sequences
38 NUMBER OF SEQUENCES: 8
39 CORRESPONDENCE ADDRESS:
40 ADDRESSEE: ONYX Pharmaceuticals, Inc.
41 STREET: 4041 Research Drive
42 CITY: Richmond
43 STATE: California
44 ZIP: 94806
45 COMPUTER READABLE FORM:
46 MEDIUM TYPE: Floppy disk
47 OPERATING SYSTEM: PC-DOS/MS-DOS
48 SOFTWARE: Patent In Release #1.0, Version #1.40
49 CURRENT APPLICATION DATA:
50 APPLICATION NUMBER: US/09/546,224
51 FILING DATE: US/09/546,224
52 CLASSIFICATION:
53 PRIOR APPLICATION DATA:
54 APPLICATION NUMBER: US 60/029,409
55 FILING DATE: 05 SEP 1996
56 ATTORNEY/AGENT INFORMATION:
57 NAME: Gloria, Gregory J.
58 REGISTRATION NUMBER: 42,028
59 REFERENCE/DESKET NUMBER: ONYX404
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: 510-222-9700
62 TELEFAX: 510-222-9758
63 INFORMATION FOR SEQ ID NO: 5:
64 SEQUENCE CHARACTERISTICS:
65 LENGTH: 2799 base pairs
66 TYPE: nucleic acid
67 TOPOLOGY: double
68 MOLECULE TYPE: cDNA (clonally)
69 HYDROTICAL: NO
70 ANTI-SENSE: NO
71 FEATURE:
72 NAME/KEY: CDS
73 LOCATION: 1..2799
74 US-08-968-752B-5

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1 TYPE: nucleic acid
2 STRANDEDNESS: double
3 TOPOLOGY: linear
4 MOLECULE TYPE: cDNA
5 HYDROTICAL: NO
6 ANTI-SENSE: NO
7 FEATURE:
8 NAME/KEY: CDS
9 LOCATION: 1..4222
10 US-09-546-224-1
11
12 Query Match
13 best Local Similarity 62.48; Pval 8e-007;
14 Matches 68; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
15
16 QY 2127 TATTTATGTTTAAACAAGATGATGCTGATGATGAGTAAATATATATGATGCTG 2186
17 DB 2675 TTATCTATGTCACAGCAACTGTTTAATGCTGTATGATTAACATGTTATTAAGCTG 2714
18
19 QY 2187 GCAACAATCAACATGATCAATGATGCTGTAGATGATGCAAAATAGC 4245
20 DB 2745 GCAACAATCAACATGATGATGCTGTGGAAGATGCTGCAAAATAGC 2783
21
22 RESULT 14
23 US-08-968-752B-5
24 Sequence 1, Application US/09536224
25 Patent No. 6479665
26 GENERAL INFORMATION:
27 APPLICANT: Frohman, Michael A.
28 APPLICANT: Morris, Andrew
29 TITLE OF INVENTION: DNA Sequences
30 NUMBER OF SEQUENCES: 8
31 CORRESPONDENCE ADDRESS:
32 ADDRESSEE: ONYX Pharmaceuticals, Inc.
33 STREET: 4041 Research Drive
34 CITY: Richmond
35 STATE: California
36 ZIP: 94806
37 COMPUTER READABLE FORM:
38 MEDIUM TYPE: Floppy disk
39 OPERATING SYSTEM: PC-DOS/MS-DOS
40 SOFTWARE: Patent In Release #1.0, Version #1.40
41 CURRENT APPLICATION DATA:
42 APPLICATION NUMBER: US/08/968,752B
43 FILING DATE: 14 Oct 1997
44 CLASSIFICATION:
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: US 60/029,409
47 FILING DATE: 05 SEP 1996
48 ATTORNEY/AGENT INFORMATION:
49 NAME: Gloria, Gregory J.
50 REGISTRATION NUMBER: 42,028
51 REFERENCE/DESKET NUMBER: ONYX404
52 TELECOMMUNICATION INFORMATION:
53 TELEPHONE: 510-222-9700
54 TELEFAX: 510-222-9758
55 INFORMATION FOR SEQ ID NO: 5:
56 SEQUENCE CHARACTERISTICS:
57 LENGTH: 2799 base pairs
58 TYPE: nucleic acid
59 TOPOLOGY: double
60 MOLECULE TYPE: cDNA (clonally)
61 HYDROTICAL: NO
62 ANTI-SENSE: NO
63 FEATURE:
64 NAME/KEY: CDS
65 LOCATION: 1..2799
66 US-08-968-752B-5

```


DR 101: 1997:47:462/44.
 XX P-PSB; A062511.
 PT recombinant Ricinus communis phospholipase D gene - which hydrolyses
 PT phospholipid(s) to produce phosphatidic acid and trans-phosphatidyl
 PT derivatives
 XX Claim 6: Columns 11-14: 14pp: English.
 XX The present sequence encodes a cationic bean phospholipase D (PLD),
 XX which hydrolyses phospholipids to produce phosphatidic acid and
 XX transphosphatidyl derivatives.
 CC A lambda Zap cDNA library from castor bean endosperm was screened
 CC with pLD cDNA specific probes. Clones that hybridised with both
 CC probes were excised in vivo with helper phage 8144 in plasmid
 CC SK(-). Both ends of the inserts were sequenced. The deduced amino
 CC acid sequence from 1 clone matched the amino-terminal sequence of
 XX purified Ricinus communis PLD.

SQ Sequence 2834 BP: 815 A: 550 C: 668 G: 801 T: 0 other:

Query Match: 97.2% Score 2728.4; DB 18: Length 2834;

Best Local Similarity 99.1% Ident: 80; 0;

Matches: 279; Conservative: 0; Mismatches: 21; Indels: 4;

1 CTTGCTTCACATCTCTGATTTTATGACATGAGTATGATGAAATATTATTGAT 60

9 CTTGCTTCACATCTCTGATTTTATGACATGAGTATGATGAAATATTATTGAT 68

61 AT 120

62 AT 128

121 CTTGCTTCACATCTCTGATTTTATGACATGAGTATGATGAAATATTATTGAT 180

129 CTTGCTTCACATCTCTGATTTTATGACATGAGTATGATGAAATATTATTGAT 188

181 GATGAGATCTAT 240

189 GATGAGATCTAT 248

241 GATGAGATCTAT 300

249 GATGAGATCTAT 308

401 GATGAGATCTAT 460

409 GATGAGATCTAT 468

401 GATGAGATCTAT 420

409 GATGAGATCTAT 428

421 GATGAGATCTAT 480

429 GATGAGATCTAT 488

481 GATGAGATCTAT 540

489 GATGAGATCTAT 548

541 GATGAGATCTAT 600

549 GATGAGATCTAT 608

601 GATGAGATCTAT 660

609 GATGAGATCTAT 668

661 GATGAGATCTAT 720

669 GATGAGATCTAT 728

721 TCTGAT 780
 729 TCTGAT 788
 781 GCTGAT 840
 789 GCTGAT 848
 841 GCTGAT 900
 849 GCTGAT 908
 901 GCTGAT 960
 909 GCTGAT 968
 961 GCTGAT 1020
 969 GCTGAT 1028
 1021 GCTGAT 1080
 1029 GCTGAT 1088
 1081 GCTGAT 1140
 1089 GCTGAT 1148
 1141 GCTGAT 1200
 1149 GCTGAT 1208
 1201 GCTGAT 1260
 1209 GCTGAT 1268
 1261 GCTGAT 1320
 1269 GCTGAT 1328
 1321 GCTGAT 1380
 1329 GCTGAT 1388
 1381 GCTGAT 1440
 1389 GCTGAT 1448
 1441 GCTGAT 1500
 1449 GCTGAT 1508
 1501 GCTGAT 1560
 1509 GCTGAT 1568
 1561 GCTGAT 1620
 1569 GCTGAT 1628
 1621 GCTGAT 1680
 1629 GCTGAT 1688
 1681 GCTGAT 1740
 1689 GCTGAT 1748
 1741 GCTGAT 1800
 1749 GCTGAT 1808

Matches	658:	Conservative	0:	Mismatches	197:	Indels	0:	Gaps	0:
UY	1743	TTGTTGGAGTCTGATGATGATTAAGAGTGGAGATTAATGATGATTAAGACTTA	1802						
DB	1	TT	60						
UY	1803	AGGAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1802						
DB	61	AAAGTTTGCTGGAGCAATAGTAGAAGATTAAGATTAAGATTAAGATTAAGATTA	120						
UY	1803	TTTCTGTTGTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATG	1922						
DB	122	TT	180						
UY	1923	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1982						
DB	181	TT	240						
UY	1983	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2042						
DB	241	TT	300						
UY	2043	TTTAAAGAGTGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2102						
DB	301	TT	360						
UY	2103	GAATTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2162						
DB	461	TT	420						
UY	2163	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2222						
DB	421	TT	480						
UY	2223	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2282						
DB	481	TT	540						
UY	2283	GAATTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2342						
DB	541	TT	600						
UY	2343	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2402						
DB	601	TT	660						
UY	2403	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2462						
DB	661	TT	720						
UY	2463	GAATTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2522						
DB	721	TT	780						
UY	2523	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2582						
DB	781	TT	840						
UY	2583	CAATTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2597						
DB	841	TT	855						

BMS017.7
 AACQ246
 AN4246 standard; DNA: 4216 BP.
 AAC246
 17-oct-2000 (11:51:00) (Y)
 Arabidopsis thaliana DNA treatment SEQ ID No: 47455.

Matches	658:	Conservative	0:	Mismatches	197:	Indels	0:	Gaps	0:
UY	1743	TTGTTGGAGTCTGATGATGATTAAGAGTGGAGATTAATGATGATTAAGACTTA	1802						
DB	1	TT	60						
UY	1803	AGGAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1802						
DB	61	AAAGTTTGCTGGAGCAATAGTAGAAGATTAAGATTAAGATTAAGATTAAGATTA	120						
UY	1803	TTTCTGTTGTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATG	1922						
DB	122	TT	180						
UY	1923	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1982						
DB	181	TT	240						
UY	1983	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2042						
DB	241	TT	300						
UY	2043	TTTAAAGAGTGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2102						
DB	301	TT	360						
UY	2103	GAATTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2162						
DB	461	TT	420						
UY	2163	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2222						
DB	421	TT	480						
UY	2223	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2282						
DB	481	TT	540						
UY	2283	GAATTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2342						
DB	541	TT	600						
UY	2343	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2402						
DB	601	TT	660						
UY	2403	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2462						
DB	661	TT	720						
UY	2463	GAATTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2522						
DB	721	TT	780						
UY	2523	ATTTGTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2582						
DB	781	TT	840						
UY	2583	CAATTAAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	2597						
DB	841	TT	855						

BMS017.7
 AACQ246
 AN4246 standard; DNA: 4216 BP.
 AAC246
 17-oct-2000 (11:51:00) (Y)
 Arabidopsis thaliana DNA treatment SEQ ID No: 47455.

[illegible]

28-047-1999; 9405-0161217H,
(WNT) UNIV NORTH TEXAS,
Chapman Rd., Aust In Brown St;
WPI: 2001-355165/47.
P-PUB: AAH96024.

Composition useful for prolonging freshness or aesthetic appearance of a plant, flower, fruit, or plant cutting comprises an N-acetylaniline compound and a horticulturally acceptable vehicle -

Claim 51: Page 9; 12pp; English.

The present invention describes a composition (1) comprising a first N-acetylaniline compound and a second N-acetylaniline compound that provides an aesthetic appearance of a plant, flower, fruit, or plant cutting and a horticulturally acceptable vehicle, (1) or a solution comprising the N-acetylaniline compound is useful for delaying the senescence of a plant selected from roses, gerberas, tulips, daffodils, hyacinths, carnations, chrysanthemums, baby's breath, daisies, gladioli, iris, peonies, delphiniums, larkspur, lisianthus, statice, snapdragons, dentonias, sunflowers, snap dragons, and ornamental foliage, preferably foliage where the ornamental foliage comprises cut leaves, stalks, stems, branches, limbs, or cut trees, or ornamental clustemas, halcy plants, bracteas, or arbutus), flower, fruit, or plant cutting, the plant being such as a bulb, bloom, bud, flower, petal, stem, branch, rhizome, root, seedling, or plantlet, wherein the composition comprising the first and second N-acetylaniline compounds promotes the delayed cultivation of plant, delaying senescence prior to harvest, thereby increasing the tolerance, freshness, or aesthetic characteristics, reduces the drop, wilt, bloom loss, needle drop, or care of dehydration, of plant, flower, fruit, or plant cutting, or prolongs or extends the appearance, texture, taste, quality, shelf life, transportability, or storability of fruit.

The present sequence encodes the specifically claimed tobacco biosynthetic pathway (240) but a protein, which is used in an example from the present invention for the production of active rib in E. coli.

Sequence 1174 BP; 468 A; 245 G; 268 G; 302 T; 0 other;

[illegible][illegible]

2025-09-11 14:11:11

RECEIVED
JAN 20 1964

[illegible]

... 11

X

ALLY

XX

DT 28-AN

XX

DE: Liquid

XX

KW MSS

nicoli Mx

KW 1.4115

KW 11111111

KW
b:est

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleotide - nucleotide search, using sw model

Run on: May 4, 2003, 21:56:05 ; Search time 8180.21 Seconds
(without alignments)
9751.626 Million cell updates/sec
Title: US-09-817-869-2
Perfect score: 2808
Sequence: 1 cttcttttcacattctctgt.....cattgttttttctacaaac 2408

Scoring table: IDENTITY_NMC
Gapop 10.0 ; Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match, 0%

Maximum Match 100%

Listing first 45 summaries

Database :

General: *

1: qb.ba: *

2: qb.ba: *

3: qb.ba: *

4: qb.in: *

5: qb.ov: *

6: qb.pat: *

7: qb.ph: *

8: qb.ph: *

9: qb.pr: *

10: qb.ro: *

11: qb.sts: *

12: qb.sts: *

13: qb.un: *

14: qb.vl: *

15: en.ba: *

16: en.hum: *

17: en.hum: *

18: en.in: *

19: en.in: *

20: en.mus: *

21: en.or: *

22: en.ov: *

23: en.pat: *

24: en.ph: *

25: en.pl: *

26: en.ro: *

27: en.sts: *

28: en.sts: *

29: en.un: *

30: en.htg.hum: *

31: en.htg.in: *

32: en.htg.other: *

33: en.htg.mus: *

34: en.htg.pln: *

35: en.htg.ro: *

36: en.htg.sts: *

37: en.htg.un: *

38: en.sy: *

39: en.htg.hum: *

40: en.htg.mus: *

41: en.htg.other: *

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Query length	DB ID	Description
1	2808	100.0	2808	8	RCOPLD
2	2728.4	97.2	2834	6	L4666 Nicotiana glauca
3	1652.8	57.7	2976	8	166478 Sequence 1
4	1652.8	57.9	2976	8	Nicotiana glauca
5	1559.8	56.6	2723	8	Nicotiana glauca
6	1559.2	56.6	2697	8	Nicotiana glauca
7	1574.8	56.1	2427	8	AF013252 Lycopersicon
8	1509	53.7	2856	8	AF006438 Arabidopsis
9	1426.8	50.8	2674	8	AF013401 Arabidopsis
10	1415.8	50.4	2794	8	AF013401 Arabidopsis
11	1415.8	50.4	2794	8	AF013401 Arabidopsis
12	1411.4	50.3	2702	8	AF000444 Arabidopsis
13	1405	50.0	2848	8	AF154425 Lycopersicon
14	1397.2	49.8	2793	8	AF000445 Arabidopsis
15	1380.4	49.2	81370	8	AB017071 Arabidopsis
16	1373.8	48.9	2590	8	AF000402 Arabidopsis
17	1373.8	48.9	3040	6	AB005011 Arabidopsis
18	1373.8	48.9	3040	6	AB005011 Arabidopsis
19	1373.8	48.9	3040	6	AB005011 Arabidopsis
20	1360.6	48.5	2862	8	AF013400 Arabidopsis
21	1345	47.9	117747	8	AF000402 Arabidopsis
22	1340.4	47.7	2829	8	AF013253 Lycopersicon
23	1330.4	47.4	2793	8	AF000402 Arabidopsis
24	1330.4	47.4	2804	6	AB005012 Arabidopsis
25	1276.8	45.5	2903	8	AF013254 Lycopersicon
26	1276.8	45.5	2903	8	AF013254 Lycopersicon
27	1235.6	43.1	14525	2	AF0122167 Arabidopsis
28	1124.2	40.0	5671	8	AF000420 Arabidopsis
29	1115	39.7	4614	8	AF113919 Arabidopsis
30	1106.2	39.4	1875	8	AF451460 Arabidopsis
31	1093.4	38.9	1518	8	AF451479 Arabidopsis
32	1092.6	38.9	3404	8	AF113918 Arabidopsis
33	1050	37.4	2397	8	AF451491 Arabidopsis
34	1050	37.4	2397	8	AF451491 Arabidopsis
35	891.8	31.8	148054	2	AF007553 Arabidopsis
36	848.8	29.9	2067	8	AF451482 Arabidopsis
37	758.6	27.0	148906	2	AF003429 Arabidopsis
38	739.2	26.3	5169	8	AB001919 Arabidopsis
39	624.5	22.2	4740	8	AF271457 Arabidopsis
40	590.4	21.0	6672	8	AF271456 Arabidopsis
41	585.6	20.9	148906	2	AF003429 Arabidopsis
42	484.6	17.1	148906	2	AF003429 Arabidopsis
43	459.2	16.4	4308	8	AF003429 Arabidopsis
44	451.2	16.1	110619	8	AF006458 Arabidopsis
45	44.9	16.0	3043	8	AF013256 Lycopersicon

ALIGNMENTS

RESULT 1

LOCUS	RCOPLD	2808 bp	mRNA	linear	PLN 19-JUL-1996
DEFINITION	Nicotiana glauca	complete cds.			
ACCESSION	L33686.1				
VERSION	L33686.1				
KEYWORDS	phospholipase D				
SOURCE	Nicotiana glauca				
ORGANISM	Nicotiana glauca (strain halo)				
REFERENCE	1 (bases 1 to 2808)				
AUTHORS	Wang, X., Xu, L. and Zhou, L.				
TITLE	Cloning and expression of phosphatidylcholine hydrolyzing				

Db 460 TTCAATATTTTGGCTATCTGGCTTCAATAATATTAATTAATCTGCGAAAGATGATC 519
 QY 459 CTATGGGTCACCTTAATGGACAGATATATGCTAGCTGAAGAGCTGTAGATGAG 518
 Db 520 QVATGGGGCAGCACTAATGGAGAGCAATGTCGCACTTTCTGAGGTTCGTGAGTGGCC 579
 QY 519 AAGAGATAGTAGGTGGTTCAGATATTTGGATGAAGACAGAGACCGCTGCATAGCTGT 578
 Db 580 ATGAAGATAGTAAATGGGTGAAATCTTGACACAGACAGAAACCCCAATAGAGGGGTT 639
 QY 579 GTAGAGATAGTAAATGAGCTAACTTTTGAATGATACGAGAGAGAGAGAGAGAGAG 638
 Db 640 CAAGATCATGTCGAGGCTGCAATATTTGATGTCTAAAGACAGCCAACTGGCGAGAG 699
 QY 639 GTATCAGAAATCAAAATATCTGGATAGCTTATATATCTCTGTCAGACAGAGAT 698
 Db 700 GAATCAAGATCAAAATACCTGGATTCGCTATACTTTCTTCAGAGAGAGAGAT 759
 QY 699 GTAGGTCTCTCTCAAAATGCTCATATGACACAAATTTCTTTCTCAAAATGCTG 758
 Db 760 GTAAAGTATTTCTGTACCAAGATGCTCATGTACCTGATCAACTTTGCTTAAATATCTC 819
 QY 759 TTTCTGAGGCAATATATGAGATGTCAGAGTGTGGTGGGAGATGTTTTGATGCAATTA 818
 Db 820 TTTCTGAGATGAGAACTATGAGGCTCATAGTGTGAGAGATATATTTGATGCAATCA 879
 QY 819 CCAATGCAAAACACATGATCATCACTGCTGCTGTGTATATCTGAAATCTGCTTAA 878
 Db 880 CTAATGCAAAACATGATATGATCATTAATGCTGTGTGTGTATTTAGTCAAAATTCCTTGA 939
 QY 879 TAAGGATCTGAGAGAGCAAAAGCCAGAGAGATATCACTAGGTGAGCTGCTTAAGA 938
 Db 940 TAAGGATCTGAGGAG 999
 QY 939 AGAAGCAAGTGAAGAGTGTAGGTGCTTATGCTGTGTGGATGACAGAGCTGCTGTG 998
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 QY 999 GTTATTCGAAAGATGATTCATGCACTGATGATGAGGAGCACTGAACATTTCTTCC 1058
 Db 1060 GTTGTGTGAAAGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1119
 QY 1059 AGAATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1118
 Db 1120 GGGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1179
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 Db 1180 TTCAGATTTCAAAATTTTACATGCTTTACTCATGACAGAGAGATGCTGCTGCTGCTGCT 1239
 QY 1179 GTTCAAGCTTAAAT---GGACATGCGAGAGAGAGAGATTTGCTGCTGCTGCTGCTGCTG 1235
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 QY 1236 GTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1295
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 QY 1416 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1475
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 QY 1596 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1655
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 QY 1656 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1715
 Db 1720 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1779
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 Db 1780 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1839
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 Db 1840 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1899
 QY 1836 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1895
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 Db 2140 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2199
 QY 2136 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2195
 Db 2200 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2259
 QY 2196 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2255
 Db 2260 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2319
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 Db 2320 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2379
 QY 2316 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2375
 Db 2380 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2439
 QY 2376 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2435
 Db 2440 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2499
 QY 2436 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2495
 Db 2500 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2559
 QY 2496 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2555
 Db 2560 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2619
 QY 2556 AGGATGGAATGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2615
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[illegible]

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DB 42562 CTGGAGAAAGCTTATGAGAACTTTCTGATATATTAAGTTTGATGATATGAGAAAT 42623
1111 11 11 11111111 11 111111 1111 111 11 11 11 11 11
0Y 2486 GAAT 2445
1111 11 11 11 111111 11 111111 111 111 1111111111
DB 42622 TAAGGCTATTTCTGAT 42681
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0Y 2446 ATGAGTAT 2505
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DB 42682 TGTGAT 42741
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0Y 2506 CTTGAGAAAGCTTATGAGAAAGCTTATGAGAAAGCTTATGAGAAAGCTTATGAGAA 2565
11 11 11 11 111111 1111 111 11 11 11 11 11 11 11 11
DB 42742 TATGAGAAAGCTTATGAGAAAGCTTATGAGAAAGCTTATGAGAAAGCTTATGAGAA 42801
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0Y 2566 CTTGAGAAAGCTTATGAGAAAGCTTATGAGAAAGCTTATGAGAAAGCTTATGAGAA 2597
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Search completed: May 5, 2003, 05:41:48
Job time : 8468.21 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2003, 22:40:50 ; Search time 98.1203 Seconds
(without alignments)
9429.336 Million cell updates/sec

Title: US-09-817-869-1
Percent score: 783
Sequence: 1 ttttcaadgaaccagatg.....tcagaccatcatcaggtl 783

Scoring table: IDENTITY_NMC
Gapop 10.0 , Gapext 1.0

Searched: 746064 seqs, 540810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum hit seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Score 100%

Listing first 45 summaries

Database : Published Applications NA *

- 1: /cqn2_5/prodata/2/pubna/US07_PUBCOMB.seq *
- 2: /cqn2_5/prodata/2/pubna/PCT_NEW_PUB.seq *
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- 14: /cqn2_5/prodata/2/pubna/US60_PUBCOMB.seq *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	783	100.0	783	9	US-09-817-869-1
2	545.6	68.4	1052	9	US-09-770-445-144
3	489.6	62.5	2808	9	US-09-817-869-2
4	489.6	62.5	2808	9	US-09-817-869-2
5	428.2	54.7	2957	9	US-10-078-770-125
6	197	25.2	2571	9	US-09-938-842A-487
7	173	22.1	2797	9	US-10-078-770-133
8	166.4	21.3	271	10	US-09-878-574-941
9	136.4	17.4	261	10	US-09-878-574-9427
10	128.4	16.4	252	10	US-09-878-574-9427
11	101.6	13.2	833	10	US-09-770-445-688
12	83.4	10.7	856	9	US-10-078-770-145
13	83.4	10.7	856	9	US-10-078-770-145
14	82.2	10.5	357	9	US-10-078-770-127
15	76.2	9.7	152	10	US-09-878-574-6135
16	47.8	6.1	1070	10	US-09-770-445-134
17	41.8	5.3	415	10	US-09-960-352-6040
18	41.4	5.2	434	10	US-09-960-352-7449
19	37.6	4.8	5727	9	US-09-896-544-18

C	20	47.6	4.8	6757	9	US-09-896-544-14	Sequence 16, Appl
	21	37.6	4.8	7246	9	US-09-896-544-14	Sequence 19, Appl
	22	37.6	4.8	8272	9	US-09-896-544-17	Sequence 17, Appl
	23	37.2	4.8	671	9	US-10-184-644-346	Sequence 46, Appl
	24	36.2	4.6	7256	9	US-09-896-544-14	Sequence 16, Appl
	25	36.2	4.6	7256	9	US-09-896-544-21	Sequence 21, Appl
	26	36.2	4.6	7649	9	US-09-896-544-21	Sequence 21, Appl
	27	34.8	4.4	515	9	US-10-184-644-76	Sequence 76, Appl
	28	34.8	4.4	515	9	US-10-184-644-76	Sequence 76, Appl
	29	33.8	4.3	2229	10	US-09-815-242-6547	Sequence 4547, Ap
	30	33.8	4.3	2229	10	US-09-815-242-6547	Sequence 4547, Ap
	31	32.8	4.3	1184	9	US-10-134-055-419	Sequence 419, Ap
	32	32.8	4.3	1184	9	US-10-134-055-419	Sequence 419, Ap
	33	32.2	4.1	345	10	US-09-770-791-771	Sequence 771, Ap
	34	32.2	4.1	1070	10	US-09-770-445-145	Sequence 145, Ap
	35	32	4.1	1024	9	US-10-134-155-198	Sequence 198, Ap
	36	32	4.1	1824	10	US-09-815-242-9694	Sequence 9694, Ap
	37	32	4.1	14955	10	US-09-861-527A-1	Sequence 1, Appl
	38	31.8	4.1	760	10	US-09-864-864-13	Sequence 13, Appl
	39	31.8	4.1	760	10	US-09-864-864-13	Sequence 13, Appl
	40	31.4	4.0	1744	10	US-09-894-682-78	Sequence 78, Appl
	41	31.2	4.0	811	9	US-10-184-644-414	Sequence 414, Appl
	42	31.2	4.0	811	9	US-10-184-644-414	Sequence 414, Appl
	43	31	4.0	390	10	US-09-864-761-28584	Sequence 28584, A
	44	31	4.0	582	10	US-09-864-761-12004	Sequence 12004, A
	45	31	4.0	792	10	US-09-896-828-458	Sequence 458, Appl

ALIGNMENTS

RESULT 1

US-09-817-869-1
: Sequence 1, Application US/09817869
: Publication No. US20030074692A1
: ORGANISM: Arabidopsis thaliana
: APPLICANT: WARE, XUEMIN
: APPLICANT: YOUNG, SANS
: TITLE OF INVENTION: DROUGHT TOLERANT PLANTS AND METHODS OF INCREASING DROUGHT TOL
: FILE REFERENCE: 40509
: CURRENT APPLICATION NUMBER: US/09817869
: NUMBER OF SEQ ID NOS: 2002-07-11
: SOFTWARE: Patent in version 4.0
: SEQ ID NO 1
: LENGTH: 783
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-817-869-1

Query Match: 100.0% Score 783; DB 9; Length 783;
Best Local Similarity: 100.0%; Prod. No. 2.40-257;
Matches 783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTTTCAAGACACAGATGTTGGAAGTCAATTTTAGTCCATTGAGAGAGC	60
DB	1	TTTTCAAGACACAGATGTTGGAAGTCAATTTTAGTCCATTGAGAGAGC	60
QY	61	TGTTTTCAGGTTTGAGTCTGGATGAATTTTGTGAAATGCTGTATATGAGTAA	120
DB	61	TGTTTTCAGGTTTGAGTCTGGATGAATTTTGTGAAATGCTGTATATGAGTAA	120
QY	121	AAGATAACATCATGATAGAGAGTATCAAGAGTCTTATATTTATCAATAGAGAGT	180
DB	121	AAGATAACATCATGATAGAGAGTATCAAGAGTCTTATATTTATCAATAGAGAGT	180
QY	181	AGCAATTCACACAGTTTAAAGACAGTATTTCTGTGAGATCTTCTCTGAGTAA	240
DB	181	AGCAATTCACACAGTTTAAAGACAGTATTTCTGTGAGATCTTCTCTGAGTAA	240
QY	241	ATGTTATTATCTTGTAGAGATCATGATGCTGATCTTAATGCTAAAAGATGCTGATCA	300
DB	241	ATGTTATTATCTTGTAGAGATCATGATGCTGATCTTAATGCTAAAAGATGCTGATCA	300


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QY 4 15-AAAGACAGCAATGTGTGGATGTCGAAATGTTTGGTTCATTCATATGAGGAGAGCTGC 63
DB 1522 TTTTATGAGCTTCAGGACAGAAATGTCAGCACTGTTTGGATTCATTAATGTGGAGCTGC 1581
QY 64 TTTTGGTTTTCCTGAGTGTGTAAGCTGCTGTGGAGAGCGGGCTTGTACATGCTGGGAAG 123
DB 1584 TTTTGGTTTTCCTGAGTGTGTAAGCTGCTGTGGAGAGCGGGCTTGTACATGCTGGGAAG 1640
QY 124 AATTCAGTTCATGAGAGATTCACAGATTCGATGATTCATTCATTCATGATCAGAGCTGTAAG 183
DB 1641 AATTCAGTTCATGAGAGATTCACAGATTCGATGATTCATTCATTCATGATCAGAGCTGTAAG 1700
QY 184 ATTTTCATTCAGTTCGAAAGAGTACTTCCTTGGGATTCCTTTTGGCTGACAGCGCATG 243
DB 1701 ATTTTCATTCATTCGAAAGAGTACTTCCTTGGGATTCCTTTTGGCTGACAGCTGATG 1760
QY 244 GTATTACTGCTGAGAGCATCATGCGCTGCATTAATGCTGACCAAGAAAGTGTGTGTGAGA 303
DB 1761 GTATTACTGCTGAGAGCATCATGCGCTGCATTAATGCTGACCAAGAGCTTCATTCATCAGA 1820
QY 304 TASTTAGCAGATTCATCAAGCAGAGAGTGTGAGGCTGTATGTTGTGTTCATATGGCC 363
DB 1821 TACTTAGCAGATTCGAGCAGAGAGAGTGTGAGGCTGTATGTTGTGTTCATATGGCC 1880
QY 364 CAGTTCAGTTCGAGCAGAGAGAGTGTGAGGCTGTATGTTGTGTTCATATGGCCAGAGCA 423
DB 1881 CAGTTCAGTTCGAGCAGAGAGAGTGTGAGGCTGTATGTTGTGTTCATATGGCCAGAGCA 1940
QY 424 TGGAGATGATGCTCAAGAGTGTGATTCAGGCTGTCAAGGCTGTTCAGAGCGCCGAGATC 483
DB 1941 TGGAGATGATGCTCAAGAGTGTGATTCAGGCTGTTCAGAGCGCTGTCAAGGCTGTCAAGTTCAGAGCTC 2000
QY 484 TACAGAGATGATGCTCAAGAGTGTGATTCAGGCTGTTCAGAGCGCTGTCAAGAGTGTGAGAGT 543
DB 2001 TACAGAGATGATGCTCAAGAGTGTGATTCAGGCTGTTCAGAGCGCTGTCAAGAGTGTGAGAGT 2060
QY 544 ATAGAGCTGTGAGAGCAAGCTGTGAGAGCTGTATATATGAGAGCGGCGAGAGCAAGCTCC 603
DB 2061 ATAGAGCTGTGAGAGCAAGCTGTGAGAGCTGTATATATGAGAGCTGTGAGAGCGGCGAGAGCAAGCTCC 2120
QY 604 ATTTATGATTTGTTGAGAGCAAGCTGTGAGAGCTGTATATATGAGAGCTGTGAGAGCTGTGAGAGT 663
DB 2121 ATTTATGATTTGTTGAGAGCAAGCTGTGAGAGCTGTATATATGAGAGCTGTGAGAGCTGTGAGAGT 2180
QY 664 GTTTGCTCAAGCAAGCTGTGAGAGCTGTATATATGAGAGCGGCTGTGAGAGCTGTGAGAGCTGTGAGAGT 723
DB 2181 GATTCGCTCAAGCAAGCTGTGAGAGCTGTATATATGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGT 2240
QY 724 GAGTGTATCAAGCAAGCTGTGAGAGCTGTATATATGAGAGCGGCTGTGAGAGCTGTGAGAGT 783
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RESULT 4
US-10-078-770-123
: Publication No. US2003003471A1
: GENBANK INFORMATION:
: APPLICANT: Fumodo, Emolayo O.
: APPLICANT: Miao, Guo-fua
: TITLE OF INVENTION: cDNAs encoding Polypeptides
: TITLE REFERENCE: BM 365,US NA
: CURRENT FILING DATE: 2002-02-19
: PRIORITY FILING DATE: 2002-02-19
: PRIORITY FILING DATE: 2000-07-12
: PRIORITY FILING DATE: 1999-07-12
: PRIORITY FILING DATE: 1999-07-12
: PRIORITY FILING DATE: 1999-09-13
: PRIORITY FILING DATE: 1999-09-13

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: PRIOR FILING DATE: 1999-10-22
: PRIOR APPLICATION NUMBER: 60/159,878
: PRIOR FILING DATE: 1999-10-22
: PRIOR APPLICATION NUMBER: 60/157,401
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/144,419
: PRIOR FILING DATE: 1999-07-12
: PRIOR APPLICATION NUMBER: 60/143,404
: PRIOR FILING DATE: 1999-07-12
: NUMBER OF SEQ ID NOS: 196
: NUMBER OF SEQ ID NOS: 196
: SEQ ID NO 121: cDNAs, Office 97
: TYPE: DNA
: LENGTH: 2736
: ORGANISM: Glycine max
: US-10-078-770-123

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Query Match 61.6% Score 482.4 E-09 Length 2736
Local Similarity 77.0% Pos. No. 3, 60,154
Matches 601: Conservative 0: Mismatches 179: Indels 1: Gaps 1:

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DB 1477 TTCTCGAGAGATGAGACAGTGTGAAGTGTTCATGTTTACAGATTCATGCTGAGCTG 1546
QY 63 CTTCTGAGTTTCCGAGTGCCTTAAATCTGCGAGAGTTCAGGCTGTACAGATTCAGAA 122
DB 1537 CTTCTGAGTTTCCGAGATTCCTTAAATCTGCGAGAGTTCAGGCTGTACAGATTCAGAA 1545
QY 124 GATAATCATATTAAGCAATGATCAAGATGTTTATATCATGCAATGAGAGTGAAG 182
DB 1596 GATAATCATATTAAGCAATGATCAAGATGTTTATATCATGCAATGAGAGTGAAG 1659
QY 183 GATTTCATCATAGTAAAGACAGATTTCTTGGAGAGTTCCTTGGAGAGTGAAGT 242
DB 1656 GATTTCATCATATTAAGATTAATATTTCTTGGAGAGTTCCTTGGAGAGTGAAGT 1715
QY 243 GGTATTCATTCAGAGATCAATGAGTGTGATTAATGTAAGAGAGTTCCTTGGAGAG 402
DB 1716 GATATTAAGCTTGAAGCATTTGAGATTTGATGATTAAGAGAGAGTTCCTTGGAGAG 1775
QY 304 ATAGTATCAAGATTCATGAGAGAGAGTTCAGGCTGTATATATATGAGAGTTCCTTGGAGAG 462
DB 1776 ATGTTGATCAAGATTCAGAGAGAGTTCAGGCTGTATATATATGAGAGTTCCTTGGAGAG 1845
QY 363 TCAGAGAGCTTCGAGAGAGAGTTCAGGCTGTATATATATGAGAGTTCCTTGGAGAG 422
DB 1836 TCAGAGAGTTCGAGAGAGAGTTCAGGCTGTATATATATGAGAGTTCCTTGGAGAG 1895
QY 423 ATGAGAGAGTTCAGAGAGAGTTCAGGCTGTATATATATGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 482
DB 1896 ATGAGAGAGTTCAGAGAGAGTTCAGGCTGTATATATATGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 1955
QY 483 GGAAGAGATTCATGAGATTCCTTGTGTTGAGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 542
DB 1956 GGAAGAGATTCATGAGATTCCTTGTGTTGAGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 2015
QY 543 TATGAGAGTTCGAGAGAGAGTTCAGGCTGTATATATGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 602
DB 2016 TATGAGAGTTCGAGAGAGAGTTCAGGCTGTATATATGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 2075
QY 603 GATTTCATGAGTTCAGAGAGAGTTCAGGCTGTATATATGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 662
DB 2076 GATTTCATGAGTTCAGAGAGAGTTCAGGCTGTATATATGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 2145
QY 663 GATTTCATGAGTTCAGAGAGAGTTCAGGCTGTATATATGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 722
DB 2136 GATTTCATGAGTTCAGAGAGAGTTCAGGCTGTATATATGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 2195
QY 723 GAGAGTTCATGAGTTCAGAGAGAGTTCAGGCTGTATATATGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 782
DB 2196 GAGAGTTCATGAGTTCAGAGAGAGTTCAGGCTGTATATATGAGAGTTCCTTGGAGAGTTCCTTGGAGAG 2255

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QY 784 T 784

DB 2279 T 2279

RESULT 5

Sequence 125, Application US/10078770

Publication No. US2003000471A1

GENERAL INFORMATION: Emolargo O.

APPLICANT: Emolargo O.

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APPLICANT: Emolargo O.

QY	94	GTTCGGGAGAGCGGCGCTGTGTATATATGGGAAGCATACATCATCTGTTAGGAGTATACAGA	151
DB	95	GTCTCGGAGAGCGGCGCTGTGTATATATGGGAAGTATATATAGTCTGCTGCTTCGGA	153
QY	152	TGCTTATCATCTCAATCAATCAAGTCTCTA	180
DB	154	TGCTTATGTTATACCATTCGAGCTGCGA	182

Search completed: May 5, 2003, 07:27:54
Job time : 107.12 secs

LOCATION: 1..1108
US-08-968-752B-3
Query Match 5.38; Score 41.8; DB 3; Length 3108;
Best Local Similarity 61.5%; Pred. No. 0.0011;
Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 610 TGAATTCAGTCCACCAAAATGATGCTGGAGGATCAATATCAATGTCGTCG 669
DB 2561 TTAATTCAGTCCACCAAAATGATGCTGGAGGATCAATATCAATGTCGTCG 2620
QY 670 CTAAATCAATCAACAGCTGATGCTGGAGGATCAATATCAATGTCGTCG 718
DB 2621 CCAACATAATCAACAGCTGATGCTGGAGGATCAATATCAATGTCGTCG 2669

RESULT 10
US-09-536-224-1
Sequence 10, Application US/09536224
Patent No. 6379655
GENERAL INFORMATION:
APPLICANT: Frohman, Michael A.
TITLE OF INVENTION: No. 6379655el Phospholipase D Polypeptide and
TITLE OF INVENTION: DNA Sequences
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94806
COMPUTER READABLE FORM:
MEDIUM TYPE: 15M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/536,224
FILING DATE: 05/09/2002
PRIORITY INFORMATION:
PRIORITY APPLICATION NUMBER: 09/468,752
ATTORNEY/AGENT INFORMATION:
NAME: Glotta, Gregory J.
REGISTRATION NUMBER: 32,028
DOCKET NUMBER: ONY2004
TELEPHONE: 510-222-9700
TELEFAX: 510-222-9758
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3108 base pairs
TYPE: nucleic acid
CYTOSINE MESS: double
TRINUCLEOTIDE:
MOLECULE TYPE: DNA (genomic)
HYDROTICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1108
US-09-536-224-3

Query Match 5.38; Score 41.8; DB 4; Length 3108;
Best Local Similarity 61.5%; Pred. No. 0.0011;
Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 610 TGAATTCAGTCCACCAAAATGATGCTGGAGGATCAATATCAATGTCGTCG 669
DB 2561 TTAATTCAGTCCACCAAAATGATGCTGGAGGATCAATATCAATGTCGTCG 2620

QY 670 CTAAATCAACAGCTGATGCTGGAGGATCAATATCAATGTCGTCG 718
DB 2621 CCAACATAATCAACAGCTGATGCTGGAGGATCAATATCAATGTCGTCG 2669

RESULT 11
US-09-107-149-18
Sequence 18, Application US/09107149
Patent No. 6274663
GENERAL INFORMATION:
APPLICANT: Frohman, Michael A.
TITLE OF INVENTION: Phospholipase D Polypeptide and
TITLE OF INVENTION: DNA Sequences
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94806
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.40
CURRENT APPLICATION NUMBER: US/09/107,149
FILING DATE: 13-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/026,469
FILING DATE: 05 SEP-1996
ATTORNEY/AGENT INFORMATION:

Query Match 5.38; Score 41.8; DB 4; Length 4114;
Best Local Similarity 61.5%; Pred. No. 0.0011;
Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 610 TGAATTCAGTCCACCAAAATGATGCTGGAGGATCAATATCAATGTCGTCG 669
DB 2726 TTAATTCAGTCCACCAAAATGATGCTGGAGGATCAATATCAATGTCGTCG 2785
QY 670 CTAAATCAACAGCTGATGCTGGAGGATCAATATCAATGTCGTCG 718
DB 2786 CCAACATAATCAATGATGCTGGAGGATCAATATCAATGTCGTCG 2844

RESULT 12
US-08-968-752B-1
Sequence 1, Application US/08968752B
Patent No. 6043073
GENERAL INFORMATION:
APPLICANT: Frohman, Michael A.
TITLE OF INVENTION: Phospholipase D Polypeptide and
TITLE OF INVENTION: DNA Sequences
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94806
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.40
CURRENT APPLICATION NUMBER: US/08/968,752B
FILING DATE: 13-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/026,469
FILING DATE: 05 SEP-1996
ATTORNEY/AGENT INFORMATION:

1 EARLIER APPLICATION NUMBER: 08/768.147
 2 EARLIER FILING DATE: 1996-12-17
 3 NUMBER OF SEQ ID NOS: 25
 4 SOURCE: BACULIN Vcr. 2.0
 5 SEQ ID NO: 16
 6 LENGTH: 1425
 7 TYPE: DNA
 8 ORGANISM: Homo sapiens
 9 FEATURE:
 10 NAME/KEY: CDS
 11 LOCATION: [64]..(2862)
 12 US-09-107-149-16

Query Match 5.28; Score 41; DB 4; Length 3425;
 Best Local Similarity 60.28; Pred. No. 0.0022;
 Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 610 TGATTATCTGCACCAAAATGATGATGTTGACATGATGATATATATGGGTCTG 669
 DB 2118 TCATCATCCACACCAAGTGTCTATGTCACATGACCGACGACATCATGTTCTG 2377
 QY 670 CTACATCAATCCACAGCTCAATGGAGGTGTCAGAGAGACTCTGAGATAGCAATG 722
 DB 2178 CAACATCATCAATGACATGAGCTTGTGGGCAATGGACACATGAGCTGGCCCTG 2430

Search completed: May 5, 2003, 07:31:46
 Job time : 72.7368 secs

[illegible]

GenBank version 5.1.5
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9M nucleic - nucleic search, using sw model

Run on: May 4, 2003, 21:56:05 ; Search time 2336.79 Seconds
(without alignments)
9751.626 Million cell updates/sec

Title: US-09-817-869-1
Perfect score: 783
Sequence: 1 tqtccaaagaccacacatg.....tcgtgcacagatccatgggt 783

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 2054640 seps, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum db seq length: 0

Maximum db seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:

1: gb-ba:

2: gb-ba:

3: gb-ba:

4: gb-ba:

5: gb-ba:

6: gb-ba:

7: gb-ba:

8: gb-ba:

9: gb-ba:

10: gb-ba:

11: gb-ba:

12: gb-ba:

13: gb-ba:

14: gb-ba:

15: gb-ba:

16: gb-ba:

17: gb-ba:

18: gb-ba:

19: gb-ba:

20: gb-ba:

21: gb-ba:

22: gb-ba:

23: gb-ba:

24: gb-ba:

25: gb-ba:

26: gb-ba:

27: gb-ba:

28: gb-ba:

29: gb-ba:

30: gb-ba:

31: gb-ba:

32: gb-ba:

33: gb-ba:

34: gb-ba:

35: gb-ba:

36: gb-ba:

37: gb-ba:

38: gb-ba:

39: gb-ba:

40: gb-ba:

41: gb-ba:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	783	100.0	2744	8	ATU16481
2	738.6	94.3	1886	8	AF428278
3	645.6	52.7	8170	8	AF000445
4	588.2	75.1	2742	8	AF000445
5	588.2	75.1	2742	8	AF000445
6	588.2	75.1	2742	8	AF000445
7	489.6	62.5	2808	8	AF005482
8	481.4	61.5	2911	8	AF005482
9	478.4	61.1	2834	8	AF005482
10	467.9	59.9	3404	8	AF113918
11	467.9	59.9	3404	8	AF113918
12	454.8	58.1	1918	8	AF451979
13	453.2	57.9	1875	8	AF451980
14	445.8	56.9	2490	8	AF000002
15	445.8	56.9	3040	8	AF005011
16	445.8	56.9	3040	8	AF005011
17	445.8	56.9	3040	8	AF005011
18	441.2	56.3	2524	8	AF005011
19	441.2	56.3	2524	8	AF005011
20	438.2	56.0	2724	8	AF005011
21	437.2	55.8	11737	8	AF005011
22	434.6	55.5	2848	8	AF154425
23	425.4	54.3	2794	8	AF005011
24	425.4	54.3	2804	8	AF005011
25	424.4	54.2	2850	8	AF005011
26	419.2	53.8	2824	8	AF005011
27	419.2	53.8	2824	8	AF005011
28	404.2	51.6	2662	8	AF005011
29	385.4	49.4	5676	8	AF005011
30	363.4	46.4	9117	2	AF122167
31	360.8	46.1	2397	8	AF451981
32	359.2	45.9	2067	8	AF451982
33	358.2	45.7	2903	8	AF001254
34	347.2	44.3	13295	8	AF001254
35	347.2	44.3	13295	8	AF001254
36	312.8	39.9	148906	2	AF001629
37	296.6	37.9	5169	8	AF001919
38	269.8	34.5	4740	8	AF271457
39	264	33.7	148054	2	AF087553
40	260.6	33.3	110459	8	AF006258
41	252.4	32.2	8672	8	AF271456
42	252.4	32.2	110459	8	AF006258
43	247.2	30.3	551	6	AF150726
44	247.2	30.3	551	6	AF150726
45	247.2	30.3	551	6	AF150726

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
ATU16481	Arabidopsis thaliana	2744 bp mRNA	U36481	GI:1297401	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	1 (bases 1 to 2794)	Dyer, J.B., Zhou, L., and Ward, X.	Cloning and Nucleotide Sequence of a cDNA (Accession No. U36481)
AF428278	Arabidopsis thaliana	2744 bp mRNA	U36481	GI:1297401	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	1 (bases 1 to 2794)	Dyer, J.B., Zhou, L., and Ward, X.	Cloning and Nucleotide Sequence of a cDNA (Accession No. U36481)
AF000445	Arabidopsis thaliana	2744 bp mRNA	U36481	GI:1297401	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	1 (bases 1 to 2794)	Dyer, J.B., Zhou, L., and Ward, X.	Cloning and Nucleotide Sequence of a cDNA (Accession No. U36481)
AF005482	Arabidopsis thaliana	2744 bp mRNA	U36481	GI:1297401	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	1 (bases 1 to 2794)	Dyer, J.B., Zhou, L., and Ward, X.	Cloning and Nucleotide Sequence of a cDNA (Accession No. U36481)
AF005482	Arabidopsis thaliana	2744 bp mRNA	U36481	GI:1297401	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	1 (bases 1 to 2794)	Dyer, J.B., Zhou, L., and Ward, X.	Cloning and Nucleotide Sequence of a cDNA (Accession No. U36481)
AF005482	Arabidopsis thaliana	2744 bp mRNA	U36481	GI:1297401	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	1 (bases 1 to 2794)	Dyer, J.B., Zhou, L., and Ward, X.	Cloning and Nucleotide Sequence of a cDNA (Accession No. U36481)
AF005482	Arabidopsis thaliana	2744 bp mRNA	U36481	GI:1297401	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	1 (bases 1 to 2794)	Dyer, J.B., Zhou, L., and Ward, X.	Cloning and Nucleotide Sequence of a cDNA (Accession No. U36481)
AF005482	Arabidopsis thaliana	2744 bp mRNA	U36481	GI:1297401	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	1 (bases 1 to 2794)	Dyer, J.B., Zhou, L., and Ward, X.	Cloning and Nucleotide Sequence of a cDNA (Accession No. U36481)
AF005482	Arabidopsis thaliana	2744 bp mRNA	U36481	GI:1297401	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	1 (bases 1 to 2794)	Dyer, J.B., Zhou, L., and Ward, X.	Cloning and Nucleotide Sequence of a cDNA (Accession No. U36481)
AF005482	Arabidopsis thaliana	2744 bp mRNA	U36481	GI:1297401	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis thaliana	1 (bases 1 to 2794)	Dyer, J.B., Zhou, L., and Ward, X.	Cloning and Nucleotide Sequence of a cDNA (Accession No. U36481)

Pred. No. is the number of results predicted by chance to have a

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[illegible][illegible]

